

FIG. 1

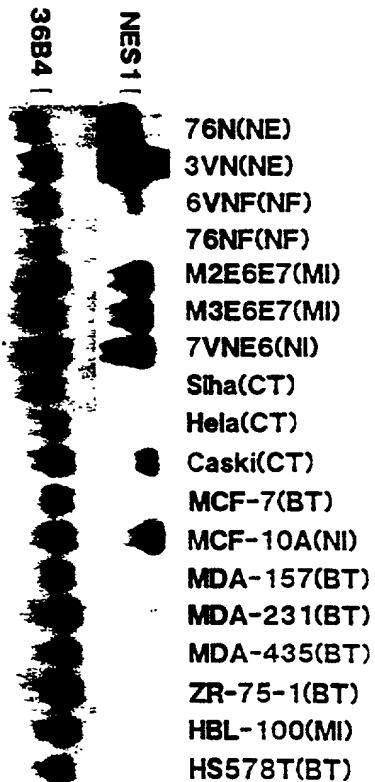


FIG. 2A

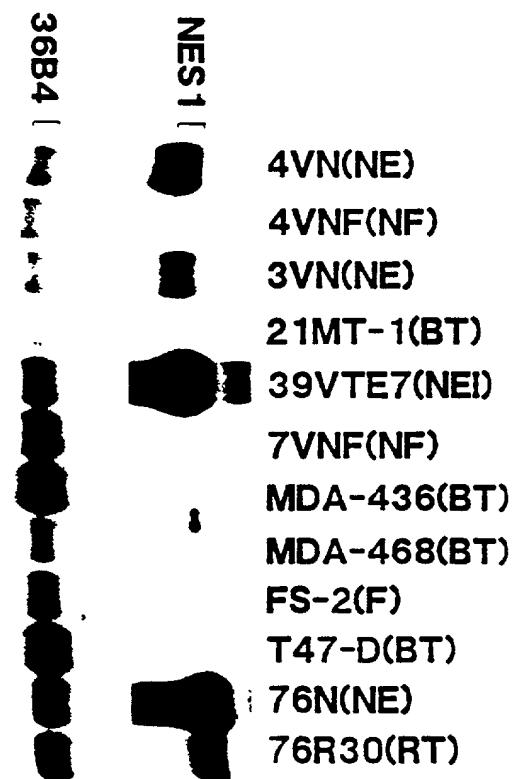
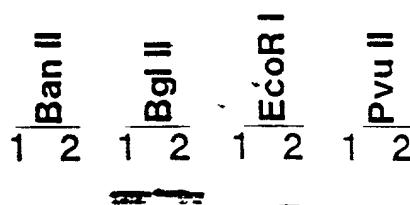
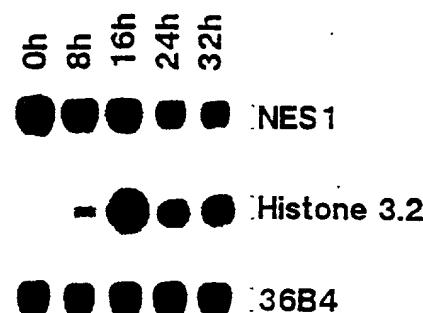
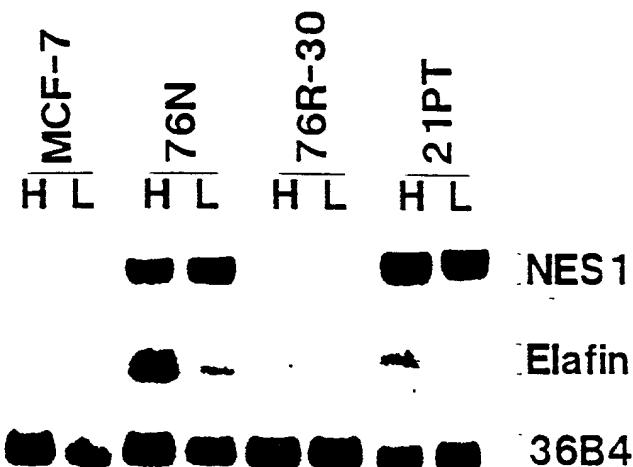
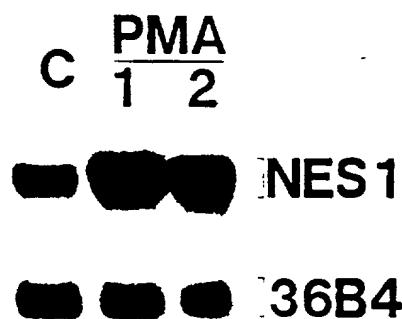
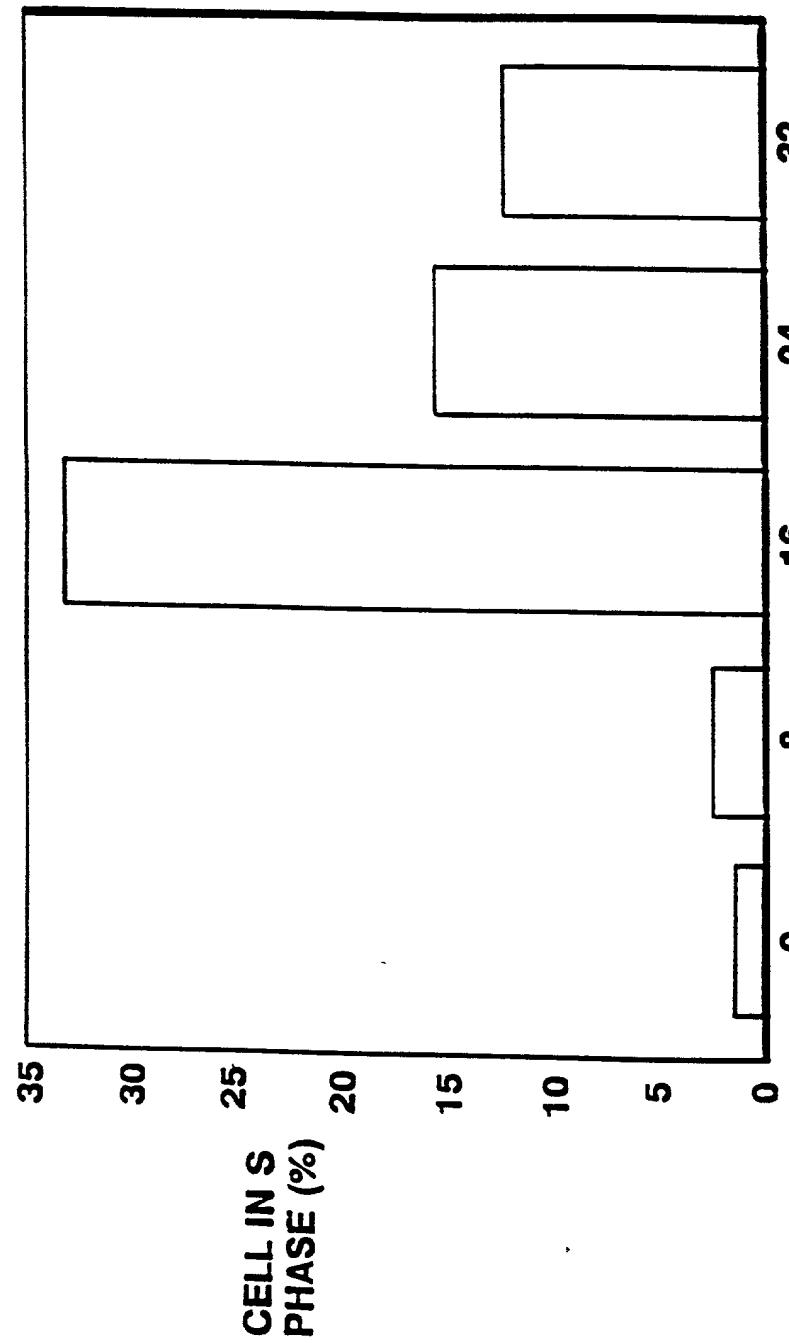


FIG. 2B

**FIG. 4****FIG. 5A****FIG. 6****FIG. 8**

**FIG. 5B**

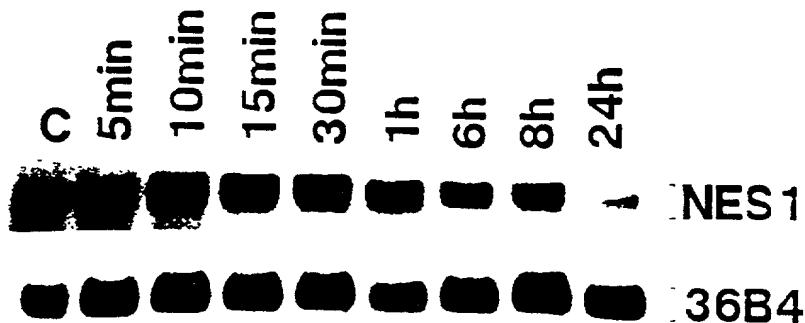


FIG. 7A

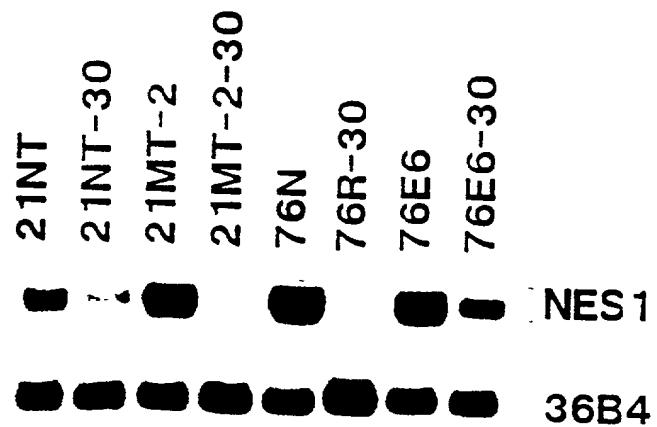


FIG. 7B

Comparison of Sequences near putative active site

	86	137	223	224	227	228	229	230	231	241	243	245
NES 1	H	D	D	P	S	D	S	G	G	G	R	W
Human Pancreatic	H	D	D	S	R	D	S	G	G	G	V	W
Trypsinogen III	▲	▲	△	△	▲	△	△	△	△	△	△	△

▲: Catalytic triad

△: Residues important for substrate binding and specificity

FIG. 9A**Alignment of NES 1 amino acid sequence with other serine proteases**

Mmtryar	1	MSALLILA LVGA.....	AVAFFVDD.D DKIVG...GY	50
Hstryivb	LELHP LLGGRTWRAA RDADGCEALG TVAVPFDD.D DKIVG...GY		
Rntrypvb		..MKICIFFT LLGT.....	VAAFPTEEDND DRIVG...GY	
Sstrypii	AAFATE..D DKIVG...GY	
Nes1		MRAPHHLHLSA ASGARALAKL LPLLMAQLWA AEAAALLPQND	<u>TRLDPEAYGA</u>	
Mmtryar	51	TCRESSVPYQ VSLNAGYHF.	CGGSLINDQW VVSAAHCYKY RIQVRLGEHN	100
Hstryivb		TC.ENSPLPYQ VSILNSGSHF.	CGGSLISEQW VVSAAHCYKT RIQVRLGEHN	
Rntrypvb		TCQEHSVPYQ VSILNAGSHI.	CGGSLIITDQW VLSAAHCYHP QLQVRLGEHN	
Sstrypii		ECKAYSQPHQ VSILNSGYHF.	CGGSLVNENW VVSAAHCYQS RVEVRLGEHN	
Nes1		PCARGSQFWQ VSIFNGLSFH	<u>CAGVLVDQSW VLTAAHCGNK PLWARVGDDH</u>	
Mmtryar	101	INVLEGNEQF VDSAKIIIRHP NYN.....	.SWTLDNDIM LIKLASPVTI	150
Hstryivb		IKVLEGNEQF INAAKIIIRHP KYN.....	.RDTLDNDIM LIKLSSPAVI	
Rntrypvb		IYEIEGAEQF IDAAKMILHP DYD.....	.KWTVDNDIM LIKLKSPATL	
Sstrypii		IQVTEGSEOF ISSSRVIRHP NYS.....	.SYNIDNDIM LIKLSKPATL	
Nes1		LLLQG. EQL RRTTRSVVHF	<u>KYHQGSGPIL PRTDEHDLM LLKLARPVVP</u>	
Mmtryar	151	NARVASVPLP SSCAPAGTQC	EXTRA INSERT	200
Hstryivb		LISGWGNTLS NGVNNPDLLQ		
Rntrypvb		NARVSTISLP TAPPAAGTEC	CVDAPVLPQA	
Sstrypii		LISGWGNTLS FGADYPDELK	CILDAPVLTQ	
Nes1		NSKVSTIPLP QYCPTAGTEC	CLDAPVLSDS	
Mmtryar		LVSGWG.VLK FGFESPSVLQ		
Hstryivb		NTYVQPVALP TSCAPAGTMC	CLNIPILSYS	
Rntrypvb		TVSGWGNTMS STAD.KNKLQ		
Sstrypii		GPRVRALQLP YRCAQPGDQC	<u>QVAGWGTTAA RRVKYNKGLT CSSITILSPK</u>	
Nes1				
Mmtryar	201	DCEASYPGDI TNNMICVGFL	250	
Hstryivb		EGGKDSCQGD SGGPVVCNGE	LQGIVSWG.Y	
Rntrypvb		EGGKDSCQRD SGGPVVCNGQ	LQGVVSWG.H	
Sstrypii		EGGKDSCQYD SGGPVVCNGE	VQGIVSWG.D	
Nes1		DCNNSYPGMI TNAMFCAGYL	LQGVVSWG.Y	
Mmtryar		EGGKDSCQGD SGGPVVCNGE	LOGILSWGIV	
Hstryivb		ECEVFYPGVV TNMNICAG.L	<u>DRGQDPQCSD SGGPLVCDET △△△</u>	
Rntrypvb				
Sstrypii				
Nes1				
Mmtryar	251	GCAQPDAPGV YTAKVCNYVDW	280	
Hstryivb		IQNTIADN*.		
Rntrypvb		GCAWKNRPGV YTAKVYNYVDW		
Sstrypii		IQDTIAANS*.		
Nes1		GCALEGKPGV YTAKVCNYLNW		
Mmtryar		IQQTVAAN*.		
Hstryivb		GCAEPGNPGV YAKCIFNDW		
Rntrypvb		LTSTMATY*.		
Sstrypii		PCGSAQHPAV YTQICKYMSW		
Nes1		INKVIRSN*.		

FIG. 9B

1 M R A P H I L S A A S G A R A L A K L L P L I M A Q L W A A E A A I L L P Q N D T R L D P E A Y G A
51 P C A R G S Q P W Q V S L F N G I S F H C A G V L V D Q S W V L T A H C G N K P L W A R V G D D H
101 I L L I Q G E Q I R R T T R S V V H P K Y H Q G S G P I L P R R T D E H D I M L L K L A R P V V P G
151 P R V R A L Q L P Y R C A Q P G D Q C Q V A G W G T T A A R R V K Y N K G L T C S S I T I L S P K E
201 C E V F Y P G V V T N N M I C A G L D R G Q D P C Q S D S G G P L V C D E T L Q G I L S W G V V P C
251 G S A Q H P A V Y T Q I C K Y M S W I N K V I R S N * (SEQ ID NO: 1)

FIG. 10

Applicant(s): Vimla Band

NES-1 POLYPEPTIDES, DNA, AND RELATED MOLECULES
AND METHODS

1 ACCAGGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCTCCCT
51 CCTTCCTATC GGCGACTCCC AGATCCTGGC CATGAGAGCT CCCCACCTCC
101 ACCTCTCCTGC CGCCTCTGGC GCCCCGGCTC TGGCGAAGCT GCTGCCGCTG
151 CTGATGGCGC AACTCTGGGC CGCAGAGGGG GCGCTGCTCC CCCAAAACGA
201 CACGGCGTTG GACCCCCGAAG CCTATGGGGC CCCGTGCGCG CGGGGCTCGC
251 AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGGGGGGGT
301 GTCCCTGGTGG ACCAGAGTTG GGTGCTGACG GCGGCGCACT GCGGAAACAA
351 GCCACTGTGG GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAAGGGCG
401 AGCAGCTCCG CCCGGACGACT CGCTCTGTTG TCCATCCCCAA GTACCACCAAG
451 GGCTCAGGCC CCATCCTGCC AAGGCCAACG GATGAGCAGC ATCTCATGTT
501 GCTAAAGCTG GCCAGGGCCCG TAGTGGGGGG GCCCCGGCTC CGGGCCCTGCC
551 AGCTTCCCTA CCGCTGTGCT CAGCCCCGAG ACCAGTGCCA GGTTGCTGGC
601 TGGGGCACCA CGGCGGGCCCG GAGAGTGAAG TACAACAAAGG GCCTGACCTG
651 CTCCAGGCATC ACTATCCTGA GCCCTAAAGA GTGTGAGGTC TTCTACCCCTG
701 GCGTGGTCAC CAACAACATG ATATGTGCTG CACTGGACCCG GGGCCAGGAC
751 CCTTGCCAGA GTGACTCTGG AGGCCCCCTG GTCTGTGACG AGACCCCTCCA
801 AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC CAGCATCCAG
851 CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA
901 CGCTCCAACG GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT
951 CCTGCTGATC CAGATGCCA GAGGCTCCAT CGTCCATCCT CTTCCCTCCCC
1001 AGTCGGCTGA ACTCTCCCT TGTCTGCACT GTTCAAACCT CTGGGGCCCT
1051 CCACACCTCT AAACATCTCC CCTCTCACCT CATTCCCCCA CCTATCCCCA
1101 TTCTCTGCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG CAAAGGTTTA
1151 TTCCAGAGAA GCCAGGAAGC CGGTCACTCAC CCAGCCTCTG AGAGCAGTTA
1201 CTGGGGTCAC CCAACCTGAC TTCCCTCTGCC ACTCCCCGCT GTGTGACTTT
1251 GGGCAAGCCA AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG
1301 GGAACAATGA CGTGCCTACC TCTTAGACAT GTTGTGAGGA GACTATGATA
1351 TAACATGTGT ATGTAAATCT TCATGTGATT GTCATGTAAG CCTTAACACA
1401 GTGGGTGGTG AGTTCTGACT AAAGGTTACC TGTGTGCGTG AAAAAAAA
1451 AAAA (SEQ ID NO: 2)

FIG. 11